

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: ABGENIX, INC.

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BLACHER, Russell Wayne
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WEBER, Richard F.
YANG, Xiao-dong

(ii) TITLE OF THE INVENTION: CD147 BINDING MOLECULES AS
THERAPEUTICS

(iii) NUMBER OF SEQUENCES: 81

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Neave
(B) STREET: 1251 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10020

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: N/A
(B) FILING DATE: 03-MAR-1999
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/034,607

(B) FILING DATE: 03-MAR-1998

(A) APPLICATION NUMBER: 09/244,253

(B) FILING DATE: 03-FEB-1999

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: ABX-CBLCD147

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ile Thr Leu Arg Val Arg Ser His

1

5

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Glu Arg Leu Arg Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Glu Arg Val Arg Trp Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Glu Arg Leu Arg Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Glu Arg Ile Arg Ser Ile

1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Glu Arg Leu Arg Ser Tyr

1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Val His Gly Asp Leu Arg Leu Arg Ser Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Asn Asp Ile Gly Leu Arg Gln Arg Ser His Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ser Pro Leu Leu Asp Gly Gln Arg Glu Arg Ser Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Tyr Asp Leu Pro Met Arg Ser Arg Ser Tyr Pro Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Xaa Arg Ser
 1

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Gly Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Arg Xaa Arg Ser His
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 269 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Ala Ala Leu Phe Val Leu Leu Gly Phe Ala Leu Leu Gly Thr
1 5 10 15
His Gly Ala Ser Gly Ala Ala Gly Thr Val Phe Thr Thr Val Glu Asp
20 25 30

Leu Gly Ser Lys Ile Leu Leu Thr Cys Ser Leu Asn Asp Ser Ala Thr
 35 40 45
 Glu Val Thr Gly His Arg Trp Leu Lys Gly Gly Val Val Leu Lys Glu
 50 55 60
 Asp Ala Leu Pro Gly Gln Lys Thr Glu Phe Lys Val Asp Ser Asp Asp
 65 70 75 80
 Gln Trp Gly Glu Tyr Ser Cys Val Phe Leu Pro Glu Pro Met Gly Thr
 85 90 95
 Ala Asn Ile Gln Leu His Gly Pro Pro Arg Val Lys Ala Val Lys Ser
 100 105 110
 Ser Glu His Ile Asn Glu Gly Glu Thr Ala Met Leu Val Cys Lys Ser
 115 120 125
 Glu Ser Val Pro Pro Val Thr Asp Trp Ala Trp Tyr Lys Ile Thr Asp
 130 135 140
 Ser Glu Asp Lys Ala Leu Met Asn Gly Ser Glu Ser Arg Phe Phe Val
 145 150 155 160
 Ser Ser Ser Gln Gly Arg Ser Glu Leu His Ile Glu Asn Leu Asn Met
 165 170 175
 Glu Ala Asp Pro Gly Gln Tyr Arg Cys Asn Gly Thr Ser Ser Lys Gly
 180 185 190
 Ser Asp Gln Ala Ile Ile Thr Leu Arg Val Arg Ser His Leu Ala Ala
 195 200 205
 Leu Trp Pro Phe Leu Gly Ile Val Ala Glu Val Leu Val Leu Val Thr
 210 215 220
 Ile Ile Phe Ile Tyr Glu Lys Arg Lys Pro Glu Asp Val Leu Asp
 225 230 235 240
 Asp Asp Asp Ala Gly Ser Ala Pro Leu Lys Ser Ser Gly Gln His Gln
 245 250 255
 Asn Asp Lys Gly Lys Asn Val Arg Gln Arg Asn Ser Ser
 260 265

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Pro Glu Arg Ile Leu Ser Ile
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly Gly Ser Arg Ala Arg Asn Leu Pro
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu Thr Asn
1 5 10 15
Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu Gln Ala
20 25 30
Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg Ile Leu
35 40 45
Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly Lys Asn
50 55 60
Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val Pro Asp

10

65 70 75 80
 Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile Glu Thr
 85 90 95
 Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu Gly Leu
 100 105 110
 Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu Ser Asp
 115 120 125
 Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp Phe Asp
 130 135 140
 Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly Ile Ile
 145 150 155 160
 Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr Gln Thr
 165 170 175
 Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp Arg Val
 180 185 190
 Val Leu Ile Gly Gly Lys Pro Asp Arg Val Val Glu Cys Ile Lys Ile
 195 200 205
 Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala Gln Pro
 210 215 220
 Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly Phe Thr
 225 230 235 240
 Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro Met Arg
 245 250 255
 Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly Arg Pro
 260 265 270
 Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg Arg Gly
 275 280 285
 Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser Arg Ala
 290 295 300
 Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly Asp Leu
 305 310 315 320
 Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp Gly Met
 325 330 335
 Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp Thr Trp
 340 345 350
 Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly Ser Gly
 355 360 365
 Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp Leu Gly
 370 375 380
 Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu Ala Gly
 385 390 395 400
 Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg His Glu
 405 410 415
 Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser Glu Asp
 420 425 430
 Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn Ala Gln
 435 440 445

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Tyr Leu Leu Gln Asn Ser Val Lys Gln Tyr Ser Gly Lys Phe Phe
 450 455 460

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30
 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 35 40 45
 Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His Tyr Ala Glu
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser
 65 70 75 80
 Val Tyr Leu Gln Met Asn Asn Leu Arg Ala Glu Asp Thr Gly Ile Tyr
 85 90 95
 Tyr Cys Thr Asp Tyr Asp Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 Val Ser Ala Glu Ser Gln Ser Phe Pro Asn Val Phe Pro Leu Val Ser
 115 120 125
 Cys Glu Ser Pro Leu Ser Asp Lys Asn Leu Val Ala Met Gly Cys Leu
 130 135 140
 Ala Arg Asp Phe Leu Pro Ser Thr Ile Ser Phe Thr Trp Asn Tyr Gln
 145 150 155 160
 Asn Asn Thr Glu Val Ile Gln Gly Ile Arg Thr Phe Pro Thr Leu Arg
 165 170 175
 Thr Gly Gly Lys Tyr Leu Ala Thr Ser Gln Val Leu Leu Ser Pro Lys
 180 185 190
 Ser Ile Leu Glu Gly Ser Asp Glu Tyr Leu Val Cys Lys Ile His Tyr
 195 200 205
 Gly Gly Lys Asn Arg Asp Leu His Val Pro Ile Pro Ala Val Ala Glu
 210 215 220

Met Asn Pro Asn Val Asn Val Phe Val Pro Pro Arg Asp Gly Phe Ser
 225 230 235 240
 Gly Pro Ala Pro Arg Lys Ser Lys Leu Ile Cys Glu Ala Thr Asn Phe
 245 250 255
 Thr Pro Lys Pro Ile Thr Val Ser Trp Leu Lys Asp Gly Lys Leu Val
 260 265 270
 Glu Ser Gly Phe Thr Thr Asp Pro Val Thr Ile Glu Asn Lys Gly Ser
 275 280 285
 Thr Pro Gln Thr Tyr Lys Val Ile Ser Thr Leu Thr Ile Ser Glu Ile
 290 295 300
 Asp Trp Leu Asn Leu Asn Val Tyr Thr Cys Arg Val Asp His Arg Gly
 305 310 315 320
 Leu Thr Phe Leu Lys Asn Val Ser Ser Thr Cys Ala Ala Ser Pro Ser
 325 330 335
 Thr Asp Ile Leu Thr Phe Thr Ile Pro Pro Ser Phe Ala Asp Ile Phe
 340 345 350
 Leu Ser Lys Ser Ala Asn Leu Thr Cys Leu Val Ser Asn Leu Ala Thr
 355 360 365
 Tyr Glu Thr Leu Asn Ile Ser Trp Ala Ser Gln Ser Gly Glu Pro Leu
 370 375 380
 Glu Thr Lys Ile Lys Ile Met Glu Ser His Pro Asn Gly Thr Phe Ser
 385 390 395 400
 Ala Lys Gly Val Ala Ser Val Cys Val Glu Asp Trp Asn Asn Arg Lys
 405 410 415
 Glu Phe Val Cys Thr Val Thr His Arg Asp Leu Pro Ser Pro Gln Lys
 420 425 430
 Lys Phe Ile Ser Lys Pro Asn Glu Val His Lys His Pro Pro Ala Val
 435 440 445
 Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala
 450 455 460
 Thr Val Thr Cys Leu Val Lys Gly Phe Ser Pro Ala Asp Ile Ser Val
 465 470 475 480
 Gln Trp Leu Gln Arg Gly Gln Leu Leu Pro Gln Glu Lys Tyr Val Thr
 485 490 495
 Ser Ala Pro Met Pro Glu Pro Gly Ala Pro Gly Phe Tyr Phe Thr His
 500 505 510
 Ser Ile Leu Thr Val Thr Glu Glu Glu Trp Asn Ser Gly Glu Thr Tyr
 515 520 525
 Thr Cys Val Val Gly His Glu Ala Leu Pro His Leu Val Thr Glu Arg
 530 535 540
 Thr Val Asp Lys Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu
 545 550 555 560
 Ile Met Ser Asp Thr Gly Gly Thr Cys Tyr
 565 570

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Lys Phe Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys
 1 5 10 15
 Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro
 20 25 30
 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr Thr
 35 40 45
 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr
 50 55 60
 Phe Thr Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys
 65 70 75 80
 Gln Gln Asp Tyr Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
 85 90 95
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
 100 105 110
 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
 115 120 125
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
 130 135 140
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
 145 150 155 160
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
 165 170 175
 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
 180 185 190
 Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser	Leu	Ala	Pro	Leu	Trp	Tyr	Tyr	Ser	Arg	His	Gly
1			5			10					

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

His	Thr	Pro	Glu	Thr	Ala	Pro	Leu	Pro	Ala	Thr	Val
1			5			10					

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

15

Met Lys Asn His Leu Leu Phe Trp Gly Val Leu Ala Val Phe Ile Lys
 1 5 10 15
 Ala Val His Val Lys Ala Gln Glu Asp Glu Arg Ile Val Leu Val Asp
 20 25 30
 Asn Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser
 35 40 45
 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val
 50 55 60
 Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
 65 70 75 80
 Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro
 85 90 95
 Thr Glu Val Glu Leu Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn
 100 105 110
 Ile Cys Asp Glu Asp Ser Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg
 115 120 125
 Asn Lys Cys Tyr Thr Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr
 130 135 140
 Lys Met Val Glu Thr Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr
 1 5 10 15
 Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro
 20 25 30
 Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr
 35 40 45
 Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr
 50 55 60
 Ser Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp
 65 70 75 80

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16

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Thr Thr Glu Tyr Tyr Tyr Tyr
 85 90 95
 Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 100 105 110
 Ser Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu
 115 120 125
 Asn Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln
 130 135 140
 Asp Phe Leu Pro Asp Xaa Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn
 145 150 155 160
 Ser Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly
 165 170 175
 Lys Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met
 180 185 190
 Gln Gly Thr Asp Glu His Val Val Thr Gly Ser Lys Glu
 195 200 205

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg
 1 5 10 15
 Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp
 20 25 30
 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
 35 40 45
 Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
 50 55 60
 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val
 65 70 75 80
 Gly Ile Tyr Tyr Cys Met Gln Thr Arg Gln Thr Pro Arg Thr Phe Gly
 85 90 95
 Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
 100 105 110

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Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser
 115 120 125
 Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Glu His
 130 135 140
 Gln Lys Ser Pro
 145

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly
 1 5 10 15
 Gly Ser Ile Ser Ser Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Pro Gly
 20 25 30
 Lys Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn
 35 40 45
 Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser
 50 55 60
 Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr
 65 70 75 80
 Ala Val Tyr Tyr Cys Ala Arg Asp Arg Gly Val Gly Ala Thr Gly Phe
 85 90 95
 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala
 100 105 110
 Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser
 115 120 125
 Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro
 130 135 140
 Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser
 145 150 155 160
 Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala
 165 170 175
 Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp
 180 185 190

Glu His Lys Val Cys
195

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ser Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Glu Arg Val Thr
1 5 10 15
Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asp Glu Leu Gly Trp Tyr
20 25 30
Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Val Ala Ser
35 40 45
Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
50 55 60
Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
65 70 75 80
Thr Tyr Tyr Cys Leu Gln His Asn Gly Tyr Pro Arg Thr Phe Gly Gln
85 90 95
Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
100 105 110
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
115 120 125
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Glu His Gln
130 135 140
Lys Ser Pro
145

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
 1 5 10 15
 Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Arg Gln Ala Thr Gly Gln
 20 25 30
 Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly
 35 40 45
 Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Asn Arg Asn Thr Ser
 50 55 60
 Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 65 70 75 80
 Ala Val Tyr Tyr Cys Ala Arg Gly Gly His Gly Gly Ser Tyr Phe Tyr
 85 90 95
 Ser Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
 100 105 110
 Ser Ser Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys
 115 120 125
 Glu Asn Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala
 130 135 140
 Gln Asp Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn
 145 150 155 160
 Asn Ser Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly
 165 170 175
 Gly Lys Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val
 180 185 190
 Met Gln Gly Thr Asp Glu His Val Val Cys Lys
 195 200

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

His Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys
 1 5 10 15
 Ser Ser Gln Ser Val Leu Tyr Ser Phe Asn Asn Lys Asn Tyr Leu Ala
 20 25 30
 Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp
 35 40 45
 Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Gly Gly Ser Gly
 50 55 60
 Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp
 65 70 75 80
 Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Arg Thr Phe
 85 90 95
 Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser
 100 105 110
 Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
 115 120 125
 Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Glu
 130 135 140
 His Gln Lys Ser Pro
 145

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
 1 5 10 15
 Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Arg Gln Ala Thr
 20 25 30
 Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn
 35 40 45

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Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asn
 50 55 60
 Thr Ser Ile Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
 65 70 75 80
 Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Glu Trp Leu Val Arg Tyr
 85 90 95
 Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 100 105 110
 Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn
 115 120 125
 Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp
 130 135 140
 Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser
 145 150 155 160
 Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
 165 170 175
 Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
 180 185 190
 Gly Thr Asp Glu His Lys Val
 195

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
 1 5 10 15
 Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Asn Leu Gly Trp Tyr
 20 25 30
 Gln Gln Lys Pro Gly Lys Ala Pro Lys Arg Leu Ile Tyr Ala Ala Ser
 35 40 45
 Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
 50 55 60
 Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 65 70 75 80

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Thr Tyr Tyr Cys Leu Gln Tyr Lys Thr Tyr Pro Trp Thr Phe Gly Gln
 85 90 95
 Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
 100 105 110
 Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
 115 120 125
 Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Xaa Lys Glu His Gln
 130 135 140
 Lys Ser Pro
 145

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Lys Leu Pro Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser
 1 5 10 15
 Phe Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly
 20 25 30
 Leu Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn
 35 40 45
 Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn
 50 55 60
 Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
 65 70 75 80
 Tyr Tyr Cys Ala Arg Gly Ala Ala Glu Tyr Tyr Tyr Tyr Tyr Gly
 85 90 95
 Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Ser
 100 105 110
 Ala Ser Ala Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro
 115 120 125
 Ser Asp Thr Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu
 130 135 140
 Pro Asp Xaa Ile Thr Phe Xaa Trp Lys Tyr Lys Asn Asn Ser Asp Ile
 145 150 155 160

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Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala
 165 170 175
 Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr
 180 185 190
 Asp Glu His Val Val Thr Gly Ser Lys Glu
 195 200

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
 1 5 10 15
 Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
 20 25 30
 Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn
 35 40 45
 Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
 50 55 60
 Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Ile
 65 70 75 80
 Tyr Tyr Cys Met Gln Ser Leu Gln Ile Pro Arg Leu Phe Gly Pro Gly
 85 90 95
 Thr Lys Val Asp Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
 100 105 110
 Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
 115 120 125
 Cys Leu Leu Ser Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
 130 135 140

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE: internal
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser
1 5 10 15
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
20 25 30
Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser
35 40 45
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
50 55 60
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
65 70 75 80
Cys Ala Arg Gly Gly Thr Thr Val Thr Phe Asp Ala Phe Asp Ile Trp
85 90 95
Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Ser Ala Ser Ala Pro
100 105 110
Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr Ser
115 120 125
Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser Ile
130 135 140
Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr Arg
145 150 155 160
Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser Gln
165 170 175
Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu
180 185 190

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser
 1      5      10      15
Gln Ser Val Leu Tyr Ser Phe Asn Asn Lys Asn Tyr Leu Ala Trp Tyr
 20     25     30
Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser
 35     40     45
Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
 50     55     60
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala
 65     70     75     80
Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Arg Thr Phe Gly Gln
 85     90     95
Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe
100     105    110
Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
115     120    125
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
130     135    140
Lys Val Ile
145

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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Asn Pro Gln Thr Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser
 1      5      10      15
Leu Ile Thr Arg Gly Val Gly Val Asp Trp Ile Arg Gln Pro Pro Gly
 20     25     30
Lys Ala Leu Gln Trp Leu Ala Leu Ile Tyr Trp Asn Asp Asp Lys Arg

```

35 40 45
 Tyr Ser Pro Ser Leu Lys Ser Arg Leu Thr Ile Thr Lys Asp Thr Ser
 50 55 60
 Lys Asn Gln Val Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr
 65 70 75 80
 Ala Thr Tyr Tyr Cys Ala His His Phe Phe Asp Ser Ser Gly Tyr Tyr
 85 90 95
 Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu Val Ser Val Ser Ser Ala
 100 105 110
 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
 115 120 125
 Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 130 135 140
 Pro Glu Pro Val Thr
 145

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Val Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala
 1 5 10 15
 Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys
 20 25 30
 Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Pro Pro Gln Leu
 35 40 45
 Leu Ile Tyr Glu Ala Phe Asn Arg Phe Ser Gly Val Pro Asp Arg Phe
 50 55 60
 Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
 65 70 75 80
 Glu Ala Glu Asp Val Gly Leu Tyr Tyr Cys Met Gln Ser Ile Glu Leu
 85 90 95
 Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val
 100 105 110
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys

27

115 120 125
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
 130 135 140
 Lys Glu Arg Val
 145

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gly Glu Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 1 5 10 15
 Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ser Met Asn Trp Val Arg Gln
 20 25 30
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ser Ile Ser Ser Ser Ser
 35 40 45
 Ser Tyr Ile Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 50 55 60
 Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg
 65 70 75 80
 Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Ser Gly Trp
 85 90 95
 Tyr Glu Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys
 115 120 125
 Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140
 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
 145 150 155 160
 Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ile
 20 25 30
 Tyr Leu Ala Trp Phe Gln Gln Arg Pro Gly Lys Ala Pro Lys Ser Leu
 35 40 45
 Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Lys Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
 65 70 75 80
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro
 85 90 95
 Phe Thr Phe Gly Pro
 100

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ile Thr Arg Gly Val Gly
 1 5 10 15

Val Asp Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Gln Trp Leu Ala
 20 25 30
 Leu Ile Tyr Trp Asn Asp Asp Lys Arg Tyr Ser Pro Ser Leu Lys Ser
 35 40 45
 Arg Leu Thr Ile Thr Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr
 50 55 60
 Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala His
 65 70 75 80
 His Phe Phe Asp Ser Ser Gly Tyr Tyr Pro Phe Asp Ser Trp Gly Gln
 85 90 95
 Gly Thr Leu Val Ser Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 100 105 110
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 115 120 125
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 130 135 140
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Gln Leu
 145 150 155

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 1 5 10 15
 Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
 20 25 30
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Thr Ile Ser Val Ser Gly
 35 40 45
 Ile Thr Thr Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 50 55 60
 Arg Asp Asn Ser Lys Asn Ile Leu Tyr Leu Gln Met Asn Ser Leu Arg
 65 70 75 80
 Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Arg Ile Phe Gly Val
 85 90 95

30

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 100 105 110
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu
 115 120 125
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 130 135 140
 Val Thr Val Ser Trp Asn Leu Gly Ala Leu Thr Ser Gly Val His Thr
 145 150 155 160
 Phe Pro Ala Val Leu Gln Ser
 165

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gly Ile Arg Leu Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser
 1 5 10 15
 Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
 20 25 30
 Ile Ser Ile Tyr Leu Ala Trp Phe Gln Gln Arg Pro Gly Lys Ala Pro
 35 40 45
 Lys Ser Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
 50 55 60
 Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 65 70 75 80
 Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
 85 90 95
 Ser Tyr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
 100 105 110
 Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln
 115 120 125
 Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140
 Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160

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Gly Lys Pro Asn

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GACTACGAAT TCTTG TAGGA CCGGC GAGGA ATAGG

35

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GACTACGGGC CCGGTGAGAA CTTGGAATCT TGCAAGC

37

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCAGTCTCCT AAAC TGCT

18

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACCTGCAAGG CCA GT

15

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CACTCATTC TGT TGAAG

18

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TCAGAAGAAG TGAAGTCAAG ATGAAGAACC ATTTGCTTTT
CTGGGGAGTC CTGGCGGTTT 60
TTATTAAGGC TGTTCATGTG AAAGCCCAAG AAGATGAAAG
GATTGTTCTT GTTGACAACA 120
AATGTAAGTG TGCCCGGATT ACTTCCAGGA TCATCCGTTC
TTCCGAAGAT CCTAATGAGG 180
ACATTGTGGA GAGAAACATC CGAATTATTG TTCCTCTGAA
CAACAGGGAG AATATCTCTG 240
ATCCACCTC ACCATTGAGA ACCAGATTTG TGTACCATTG GTCTGACCTC
TGTA AAAAAT 300
GTGATCCTAC AGAAGTGGAG CTGGATAATC AGATAGTTAC
TGCTACCCAG AGCAATATCT 360
GTGATGAAGA CAGTGCTACA GAGACCTGCT ACACTTATGA
CAGAAACAAG TGCTACACAG 420
CTGTGGTCCC ACTCGTATAT GGTGGTGAGA CCAAATGGT
GGAAACAGCC TTAACCCAG 480
ATGCCTGCTA TCCTGACTAA 500

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

34

GAATTCAGAA GAAGTGAAGT C

21

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTCGACTATG CAGTCAGCAA TGAC

24

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGCAGGAATC AGACCCAGTC

20

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

T05F20"05648260

35

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCAGGCTGG AACTGAGGAG CA

22

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TCATTTGGTG ATCAGCACT

19

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GCTAGCTGAG GAGACGGTGA CCAGG

25

(2) INFORMATION FOR SEQ ID NO:54:

T05F20"05648/60

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TCATTGTTGGTG ATCAGCACT

19

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGATCCTGAG GAGACGGTGA CG

22

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

T06T00-05648260

37

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGATTAGCAT CCGCCCCAAC CCTT

24

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTCGACGCAC ACACAGAGCG GCCA

24

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GACTACGAAT TCGGACCGGC GAGGAATAGG AATCATG

37

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGATGGTGTT GGTAGCTAGC ACGCGGAGCG TGATGATGGC CTG
43

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACTACGAAT TCACGAGGCG ACATGGCGGC GGC

33

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61

GGATGGTGTGTT GGTAGCTAGC ACACGCAGTG AGATGGTTTC CCG
43

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGACTGTTGA AGCCTTCGGA GACCCTGTCC CTCACCTGCG
CTGTCTATGG TGGGTCCTTC 60
AGTGGTACT ACTGGAGCTG GATCCGCCAG CCCCCAGGGA
AGGGGCTGGA GTGGATTGGG 120
GAAATCAATC ATAGTGGAAG CACCAACTAC AACCCGTCCC
TCAAGAGTCG AGTCACCATA 180
TCAGTAGACA CGTCCAAGAA CCAGTTCTCC CTGAAGCTGA
GCTCTGTGAC CGCNGCGGAC 240
ACGGCTGTGT ATTACTGTGC GAGAGGCACT ACGGAATATT
ACTACTACTA CTACGGTATG 300
GACGTCTGGG GCCAAGGGAC CACGGTCACC GTCTCCTCAG
GGAGTGCATC CGCCCCAACC 360
CTTTTCCCCC TCGTCTCCTG TGAGAATTCC CCGTCGGATA
CGAGCAGCGT GGCCGTTGGC 420
TGCCTCGCAC AGGACTTCCT TCCCGACTYC ATCACTTTCT CCTGGAAATA
CAAGAACAAC 480
TCTGACATCA GCAGCACCCG GGGCTTCCCA TCAGTCCTGA
GAGGGGGCAA GTACGCAGCC 540
ACCTCACAGG TGCTGCTGCC TTCCAAGGAC GTCATGCAGG
GCACAGACGA ACACGTGGTG 600
ACGGGATCCA AAGAGTA 617

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CTCTCCCTGC CCGTCACCCC TGGAGAGCCG GCCTCCATCT
CCTGCAGGTC TAGTCAGAGC 60
CTCCTGCATA GTAATGGATA CAACTATTTG GATTGGTACC
TGCAGAAGCC AGGGCAGTCT 120
CCACAGCTCC TGATCTATTT GGGTTCTAAT CGGGCCTCCG
GGGTCCCTGA CAGGTTCACT 180
GGCAGTGGAT CAGGCACAGA TTTTACACTG AAAATCAGCA
GAGTGGAGGC TGAGGATGTT 240
GGGATTTATT ACTGCATGCA GACTCGACAA ACTCCTCGGA
CGTTCGGCCA AGGGACCAAG 300
GTGGAAATCA AACGAACTGT GGCTGCACCA TCTGTCTTCA
TCTTCCCGCC ATCTGATGAG 360
CAGTTGAAAT CTGGAAGTGC CTCTGTTGTG TGCCTGCTGA
ATAACTTCTA TCCCAGAGAG 420
GCCAAAGAGC ATCAAAAGAG TCCA 444

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 593 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CTGGTGAAGC CTTCGGAGAC CCTGTCCCTC ACCTGCACTG
TCTCTGGTGG CTCCATCAGT 60
AGTTACTACT GGAAGTGGAT CCGGCAGCCC CCAGGGAAGG
GACTGGAGTG GATTGGGTAT 120
ATCTATTACA GTGGGAGCAC CAACTACAAC CCCTCCCTCA

41

AGAGTCGAGT CACCATATCA 180
GTAGACACGT CCAAGAACCA GTTCTCCCTG AAGCTGAGCT
CTGTGACCGC TGC GGACACG 240
GCCGTGTATT ACTGTGCGAG AGATAGGGGA GTGGGAGCTA
CTGGTTTTGA CTACTGGGGC 300
CAGGGAACCC TGGTCACCGT CTCCTCAGGG AGTGCATCCG
CCCCAACCT TTTCCCCCTC 360
GTCTCCTGTG AGAATTCCCC GTCGGATACG AGCAGCGTGG
CCGTTGGCTG CCTCGCACAG 420
GACTTCCTTC CCGACTCCAT CACTTTCTCC TGGAAATACA
AGAACAACCTC TGACATCAGC 480
AGCACCCGGG GCTTCCCATC AGTCCTGAGA GGGGGCAAGT
ACGCAGCCAC CTCACAGGTG 540
CTGCTGCCTT CCAAGGACGT CATGCAGGGC ACAGACGAAC
ACAAGGTGTG CGA 593

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AGCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGAGA
GAGTCACCAT CACTTGCCGG 60
GCAAGTCAGG GCATTAGAGA TGAATTAGGC TGGTATCAGC
AGAAACCAGG GAAAGCCCCT 120
AAGCGCCTGA TCTATGTTGC ATCCAGTTTG CAAAGTGGGG
TCCCATCAAG GTTCAGCGGC 180
AGTGGATCTG GGACAGAATT CACTCTCACA ATCAGCAGCC
TGCAGCCTGA AGATTTTGCA 240
ACTTATTACT GTCTACAGCA TAATGGTTAC CCTCGGACGT
TCGGCCAAGG GACCAAGGTG 300
GAAATCAAAC GAACTGTGGC TGCACCATCT GTCTTCATCT
TCCCGCCATC TGATGAGCAG 360
TTGAAATCTG GAACTGCCTC TGTGTGTGC CTGCTGAATA ACTTCTATCC
CAGAGAGGCC 420
AAAGAGCATC AAAAGAGTCC A 441

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAGAAGCCTG GGGCCTCAGT GAAGGTCTCC TGCAAGGCTT
CTGGATACAC CTTCAACAGT 60
TATGATATCA ACTGGGTGCG ACAGGCCACT GGACAAGGGC
TTGAGTGGAT GGGATGGATG 120
AACCCTAACA GTGGTAACAC AGGCTATGCA CAGAAGTTCC
AGGGCAGAGT CACCATGAAC 180
AGGAACACCT CCATAAGCAC AGCCTACATG GAGCTGAGCA
GCCTGAGATC TGAGGACACG 240
GCCGTGTATT ACTGTGCGAG AGGGGGTCAT GGTGGGAGCT
ACTTCTACTC CTAYTACGGT 300
ATGGACGTCT GGGGCCAGGG GACCACGGTC ACCGTCTCCT
CAGGGAGTGC ATCCGCCCA 360
ACCCTTTTCC CCCTCGTCTC CTGTGAGAAT TCCCCGTCGG
ATACGAGCAG CGTGGCCGTT 420
GGCTGCCTCG CACAGGACTT CCTTCCCGAC TCCATCACTT
TCTCCTGGAA ATACAAGAAC 480
AACTCTGACA TCAGCAGCAC CCGGGGCTTC CCATCAGTCC
TGAGAGGGGG CAAGTACGCA 540
GCCACCTCAC AGGTGCTGCT GCCTTCCAAG GACGTCATGC
AGGGCACAGA CGAACACGTG 600
GTGTGCAAAC 610

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CACTCCCTGG CTGTGTCTCT GGGCGAGAGG GCCACCATCA
ACTGCAAGTC CAGCCAGAGT 60
GTTTTATACA GTTTAAACAA TAAGAACTAC TTAGCTTGGT
ACCAGCAGAA ACCAGGACAG 120
CCTCCTAAGC TGCTCATTTA CTGGGCATCT ACCCGGGAAT
CCGGGGTCCC TGACCGATTC 180
GGTGGCAGCG GGTCTGGGAC AGATTTCCT CTCACCATCA
GCAGCCTGCA GGCTGAAGAT 240
GTGGCAGTTT ATTACTGTCA GCAATATTAT AGTACTCCTM
GGACGTTCGG CCAAGGGACC 300
AAGGTGGAAG TCAAACGAAC TGTGGCTGCA CCATCTGTCT
TCATCTTCCC GCCATCTGAT 360
GAGCAGTTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC
TGAATAACTT CTATCCCAGA 420
GAGGCCAAG AGCATCAAAA GAGTCCA 447

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAGGTGAAGA AGCCTGGGGC CTCAGTGAAG GTCTCCTGCA
AGGCTTCTGG ATACACCTTC 60
ACCAGTTATG ATATCAACTG GGTGCGACAG GCCACTGGAC
AAGGGCTTGA GTGGATGGGA 120
TGGATGAACC CTAACAGTGG TAACACAGGC TATGCACAGA
AGTTCCAGGG CAGAGTCACC 180
ATGACCAGGA ACACCTCCAT AAGCACAGCC TACATGGAGC
TGAGCAGCCT GAGATCTGAG 240

GACACGGCCG TGTATTACTG TGCGAGAGAG GAGTGGCTGG
TACGTTACTA CGGTATGGAC 300
GTCTGGGGCC AAGGGACCAC GGTCACCGTC TCCTCAGGGA
GTGCATCCGC CCCAACCCTT 360
TTCCCCCTCG TCTCCTGTGA GAATTCCCCG TCGGATACGA
GCAGCGTGGC CGTTGGCTGC 420
CTCGCACAGG ACTTCCTTCC CGACTCCATC ACTTTCTCCT GGAAATACAA
GAACAACCTCT 480
GACATCAGCA GCACCCGGGG CTTCCCATCA GTCCTGAGAG
GGGGCAAGTA CGCAGCCACC 540
TCACAGGTGC TGCTGCCTTC CAAGGACGTC ATGCAGGGCA
CAGACGAACA CAAGGTGTG 599

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA
GAGTCACCAT CACTTGCCGG 60
GCAAGTCAGG ACATTAGAGA TAATTTAGGC TGGTATCAGC
AGAAACCAGG GAAAGCCCCT 120
AAGCGCCTGA TCTATGCTGC ATCCAATTTG CAAAGTGGGG
TCCCATCAAG GTTCAGCGGC 180
AGTGGATCTG GGACAGAATT CACTCTCACA ATCAGCAGCC
TGCAGCCTGA AGATTTTGCA 240
ACTTATTACT GTCTACAGTA TAAAACTTAC CCGTGGACGT
TCGGCCAAGG GACCAAGGTG 300
GAAATCAAAC GAACTGTGGC TGCACCATCT GTCTTCATCT
TCCCGCCATC TGATGAGCAG 360
TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA ACTTCTATCC
CAGAGAGGMC 420
AAAGAGCATC AAAAGAGTCC A 441

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAGCTTCCGG AGACCCTGTC CCTCACCTGC GCTGTCTATG
GTGGGTCCTT CAGTGGTTAC 60
TACTGGAGCT GGATCCGCCA GCGCCAGGG AAGGGGCTGG
AGTGGATTGG GGAAATCAAT 120
CATAGTGGAA GCACCAACTA CAACCCGTCC CTCAAGAGTC
GAGTCACCAT ATCAGTAGAC 180
ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA
CCGCCGCGGA CACGGCTGTG 240
TATTACTGTG CGAGAGGGGC AGCTGAATAT TACTACTACT
ACTACGGTAT GGACGTCTGG 300
GGCCAAGGGA CCACGGTCAC CGTCTCCTCA GGGAGTGCAT
CCGCCCCAAC CCTTTTCCCC 360
CTCGTCTCCT GTGAGAATTC CCCGTCGGAT ACGAGCAGCG
TGGCCGTTGG CTGCCTCGCA 420
CAGGACTTCC TTCCCGACTY CATCACTTTC TYCTGGAAAT
ACAAGAACAA CTCTGACATC 480
AGCAGCACCC GGGGCTTCCC ATCAGTCCTG AGAGGGGGCA
AGTACGCAGC CACCTCACAG 540
GTGCTGCTGC CTTCCAAGGA CGTCATGCAG GGCACAGACG
AACACGTGGT GACGGGATCC 600
AAAGAGT 607

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ATGCCCCGTCA CCCCTGGAGA GCCGGCCTCC ATCTCCTGCA
GGTCTAGTCA GAGCCTCCTG 60
CATAGTAATG GATACAACTA TTTGGACTGG TACCTGCAGA
AGCCAGGGCA GTCTCCACAG 120
CTCCTGATCT ATTTGGGTTC TAATCGGGCC TCCGGGGTCC
CTGACAGGTT CAGTGGCAGT 180
GGATCAGGCA CAGATTTTAC ACTGAAAATC AGCAGAGTGG
AGGCTGAGGA TGTTGGGATT 240
TATTACTGCA TGCAAAGTCT ACAAATTCCC CGGCTTTTCG
GCCCTGGGAC CAAAGTGGAT 300
ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC
CGCCATCTGA TGAGCAGTTG 360
AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAGTAACT
TCTATCCCAG AGAGGCCAAA 420
GTACAGTGGA A 431

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TCGGAGACCC TGTCCTCAC CTGCGCTGTC TATGGTGGGT
CCTTCAGTGG TTACTACTGG 60
AGCTGGATCC GCCAGCCCCC AGGGAAGGGG CTGGAGTGGA
TTGGGGAAAT CAATCATAGT 120
GGAAGCACCA ACTACAACCC GTCCCTCAAG AGTCGAGTCA
CCATATCAGT AGACACGTCC 180
AAGAACCAGT TCTCCCTGAA GCTGAGTTCT GTGACCGCCG
CGGACACGGC TGTGTATTAC 240
TGTGCGAGAG GCGGGACTAC AGTAACTTTT GATGCTTTTG
ATATCTGGGG CCAAGGGACA 300

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ATGGTCACCG TCTCTTCAGG GAGTGCATCC GCCCCAACCC TTTTCCCCCT
 CGTCTCCTGT 360
 GAGAATTCCC CGTCGGATAC GAGCAGCGTG GCCGTTGGCT
 GCCTCGCACA GGA CTTCTT 420
 CCCGACTCCA TCACTTTCTC CTGGAAATAC AAGAACAAC
 CTGACATCAG CAGCACCCGG 480
 GGCTTCCCAT CAGTCCTGAG AGGGGGCAAG TACGCAGCCA
 CCTCACAGGT GCTGCTGCCT 540
 TCCAAGGACG TCATGCAGGG CACAGACGAA 570

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CTGGCTGTGT CTCTGGGCGA GAGGGCCACC ATCAACTGCA
 AGTCCAGCCA GAGTGTTT 60
 TACAGTTTTA ACAATAAGAA CTA CTTAGCT TGGTACCAGC
 AGAAACCAGG ACAGCCTCCT 120
 AAGCTGCTCA TTTACTGGGC ATCTACCCGG GAATCCGGGG
 TCCCTGACCG ATTCAGTGGC 180
 AGCGGGTCTG GGACAGATT CACTCTCACC ATCAGCAGCC
 TGCAGGCTGA AGATGTGGCA 240
 GTTTATTACT GTCAGCAATA TTATAGTACT CCTCGGACGT
 TCGGCCAAGG GACCAAGGTG 300
 GAAATCAAAC GAACTGTGGC TGCACCATCT GTCTTCATCT
 TCCCGCCATC TGATGAGCAG 360
 TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA ACTTCTATCC
 CAGAGAGGCC 420
 AAAGTACAGT GGAAGGTGAT C 441

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid

T09120"0549.650

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AACCCACAGA CGACCCTCAC GCTGACCTGC ACCTTCTCTG
GGTTCTCACT CATTACCCGT 60
GGAGTGGGTG TGGATTGGAT CCGTCAGCCC CCAGGAAAGG
CCCTGCAGTG GCTCGCACTC 120
ATTTATTGGA ATGATGATAA GCGCTACAGT CCATCTCTGA
AGAGCAGGCT CACCATCACC 180
AAGGACACCT CCAAAAACCA GGTGGTCCTC ACAATGACCA
ACATGGACCC TGTGGACACA 240
GCCACATATT ACTGTGCACA CCATTCTTT GATAGTAGTG GTTATTACCC
TTTTGACTCC 300
TGGGGCCAGG GAACCCTGGT CTCCGTCTCC TCAGCCTCCA
CCAAGGGCCC ATCGGTCTTC 360
CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG
CGGCCCTGGG CTGCCTGGTC 420
AAGGACTACT TCCCCGAACC GGTGACG 447

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GTGACTCAGT CTCCACTCTC TCTGTCCGTC ACCCCTGGAC
AGCCGGCCTC CATCTCCTGC 60
AAGTCTAGTC AGAGCCTCCT GCATAGTGAT GGAAAGACCT
ATTTGTATTG GTACCTGCAG 120

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AAGCCAGGCC AGCCTCCACA GCTCCTGATC TATGAAGCTT
TCAACCGGTT CTCTGGAGTG 180
CCAGATAGGT TCAGTGGCAG CGGGTCAGGG ACAGATTTC
CACTGAAAAT CAGCCGGGTG 240
GAGGCTGAGG ATGTTGGACT TTATTATTGC ATGCAAAGTA
TAGAGCTTCC GTTCACTTTC 300
GGCGGAGGGA CCAAGGTGGA GATCAAACGA ACTGTGGCTG
CACCATCTGT CTTATCTTC 360
CCGCCATCTG ATGAGCAGTT GAAATCTGGA ACTGCCTCTG
TTGTGTGCCT GCTGAATAAC 420
TTCTATCCCA GAAAAGAAAG AGTCR 445

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGGGAAGGCC TGGTCAAGCC TGGGGGGTCC CTGAGACTCT
CCTGTGCAGC CTCTGGATTC 60
ACCTTCAGTA GCTATAGCAT GAACTGGGTC CGCCAGGCTC
CAGGGAAGGG GCTGGAGTGG 120
GTCTCATCCA TTAGTAGTAG TAGTAGTTAC ATATACTACG
CAGACTCAGT GAAGGGCCGA 180
TTCACCATCT CCAGAGACAA CGCCAAGAAC TCACTGTATC
TGCAAATGAA CAGCCTGAGA 240
GCCGAGGACA CGGCTGTGTA TTA CTGTGCG AGGGATAGCA
GTGGCTGGTA TGAGGACTAC 300
TTTGACTACT GGGGCCAGGG AACCTGGTC ACCGTCTCCT
CAGCCTCCAC CAAGGGCCCA 360
TCGGTCTTCC CCCTGGCGCC CTGCTCCAGG AGCACCTCCG
AGAGCACAGC GGCCCTGGGC 420
TGCCTGGTCA AGGACTACTT CCCC GAACCG GTGACGGTGT
CGTGGA ACTC AGGCGCTCTG 480
ACCAGCGGCG TGCACACCTT CCCAGCTGTC CTACAGTCA
519

PCT/US99/04583

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTTGACATCC AGCTGACCCA GTCTCCGTCC TCACTGTCTG
CATCTGTAGG AGACAGAGTC 60
ACCATCACTT GTCGGGCGAG TCAGGACATT AGCATTTATT
TAGCCTGGTT TCAGCAGAGA 120
CCAGGGAAAG CCCCTAAGTC CCTGATCTAT GCTGCATCCA
GTTTGCAAAG TGGGGTCCCA 180
TCAAAGTTCA GCGGCAGTGG ATCTGGGACA GATTTCACCTC
TCACCATCAG CAGCCTGCAG 240
CCTGAAGATT TTGCAACTTA TTAGTCCAA CAATATAATA GTTATCCATT
CACTTTCGGG 300
CCC 303

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CTGACCTGCA CCTTCTCTGG GTTCTCACTC ATTACCCGTG
GAGTGGGTGT GGATTGGATC 60
CGTCAGCCCC CAGGAAAGGC CCTGCAGTGG CTCGCACTCA

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TTTATTGGAA TGATGATAAG 120
CGCTACAGTC CATCTCTGAA GAGCAGGCTC ACCATCACCA
AGGACACCTC CAAAAACCAG 180
GTGGTCCTCA CAATGACCAA CATGGACCCT GTGGACACAG
CCACATATTA CTGTGCACAC 240
CATTTCTTTG ATAGTAGTGG TTATTACCCT TTTGACTCCT
GGGGCCAGGG AACCTGGTC 300
TCCGTCTCCT CAGCCTCCAC CAAGGGCCCA TCGGTCTTCC
CCCTGGCGCC CTGCTCCAGG 360
AGCACCTCCG AGAGCACAGC GGCCCTGGGC TGCCTGGTCA
AGGACTACTT CCCC GAACCG 420
GTGACGGTGT CGTGGAAGTC AGGCGCTCTG ACCAGCGGCG
TGCACACCTT CCAGCTG 477

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGGGGAGGCT TGGTACAGCC TGGGGGGTCC CTGAGACTCT
CCTGTGCAGC CTCTGGATTC 60
ACTTTTAGCA GCTATGCCAT GAGCTGGGTC CGCCAGGCTC
CAGGGAAGGG GCTGGAGTGG 120
GTCTCAACTA TTAGTGTTAG TGGTATTACC ACATACTACG
TAGACTCCGT GAAGGGCCGG 180
TTCACCATCT CCAGAGACAA TTCCAAGAAC ATTCTGTATC
TGCAAATGAA CAGCCTGAGA 240
GCCGAGGACA CGGCCGTATA TTAGTGTGCG AAACGGATTT
TTGGAGTGGT CTGGGGCCAG 300
GGAACCCTGG TCACCGTCTC CTCAGCCTCC ACCAAGGGCC
CATCGGTCTT CCCCCTGGCG 360
CCCTGCTCCA GGAGCACCTC CGAGAGCACA GCGGCCCTGG
GCTGCCTGGT CAAGGACTAC 420
TTCCCCGAAC CGGTGACGGT GTCGTGGAAC TTAGGCGCTC
TGACCAGCGG CGTGACACAC 480
TTCCAGCTG TCCTACAGTC CTA 503

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGAATTCGGC TTGATATTCA GCTGACTCAG TCTCCATCCT CACTGTCTGC
ATCTGTAGGA 60
GACAGAGTCA CCATCACTTG TCGGGCGAGT CAGGGCATT
GCATTTATTT AGCCTGGTTT 120
CAGCAGAGAC CAGGGAAAGC CCCTAAGTCC CTGATCTATG
CTGCATCCAG TTTGCAAAGT 180
GGGGTCCCAT CAAAGTTCAG CGGCAGTGGA TCTGGGACAG
ATTTCACTCT CACCATCAGC 240
AGCCTGCAGC CTGAAGATTT TGCAACTTAT TACTGCCAAC
AATATAATAG TTACCCATTC 300
ACTTTCGGCC CTGGGACCAA AGTGGATATC AAACGAACTG
TGGCTGCACC ATCTGTCTTC 360
ATCTTCCCGC CATCTGATGA GCAGTTGAAA TCTGGAAC TG
CCTCTGTTGT GTGCCTGCTG 420
AATAACTTCT ATCCAGAGA GGCCAAAGTA CAGTGGAAGG
TGGATAACGC CCTCCAATCG 480
GGTAAGCCGA ATTC 494

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

ATGTACTTGG GACTGAACTA TGTATTCATA GTTTTTCTCT TAAATGGTGT
CCAGAGTGAA 60
GTGAAGCTTG AGGAGTCTGG AGGAGGCTTG GTGCAACCTG
GAGGATCCAT GAAACTCTCC 120
TGTGTTGCCT CTGGATTCAC TTTCAGTAAC TACTGGATGA
ACTGGGTCCG CCAGTCTCCA 180
GAGAAGGGGC TTGAGTGGGT TGCTGAAATT AGATTGAAAT
CTAATAATTA TGCAACACAT 240
TATGCGGAGT CTGTGAAAGG GAGGTTCCACC ATCTCAAGAG
ATGATTCCAA AAGTAGTGTC 300
TACCTGCAAA TGAACAACCTT AAGAGCTGAA GAACTGGCA
TTTATTACTG TACGGATTAC 360
GATGCTTACT GGGGCCAAGG GACTCTGGTC ACTGTCTCTG
CAGAGAGTCA GTCCTTCCCA 420
AATGTCTTCC CCCTCGTCTC CTGCGAGAGC CCCCTGTCTG
ATAAGAATCT GGTGGCCATG 480
GGCTGCCTGG CCCGGGACTT CCTGCCCAGC ACCATTTCCT
TCACCTGGAA CTACCAGAAC 540
AACACTGAAG TCATCCAGGG TATCAGAACC TTCCCAACAC
TGAGGACAGG GGGCAAGTAC 600
CTAGCCACCT CGCAGGTGTT GCTGTCTCCC AAGAGCATCC
TTGAAGGTTC AGATGAATAC 660
CTGGTATGCA AAATCCACTA CGGAGGCAAA AACAGAGATC
TGCATGTGCC CATTCCAGCT 720
GTCGCAGAGA TGAACCCCAA TGTAATGTG TTCGTCCCAC
CACGGGATGG CTTCTCTGGC 780
CCTGCACCAC GCAAGTCTAA ACTCATCTGC GAGGCCACGA
ACTTCACTCC AAAACCGATC 840
ACAGTATCCT GGCTAAAGGA TGGGAAGCTC GTGGAATCTG
GCTTCACCAC AGATCCGGTG 900
ACCATCGAGA ACAAAGGATC CACACCCCAA ACCTACAAGG
TCATAAGCAC ACTTACCATC 960
TCTGAAATCG ACTGGCTGAA CCTGAATGTG TACACCTGCC
GTGTGGATCA CAGGGGTCTC 1020
ACCTTCTTGA AGAACGTGTC CTCCACATGT GCTGCCAGTC
CCTCCACAGA CATCCTAACC 1080
TTCACCATCC CCCCTCCTT TGCCGACATC TTCCTCAGCA AGTCCGCTAA
CCTGACCTGT 1140
CTGGTCTCAA ACCTGGCAAC CTATGAAACC CTGAATATCT
CCTGGGCTTC TCAAAGTGGT 1200
GAACCACTGG AAACCAAAAT TAAAATCATG GAAAGCCATC
CCAATGGCAC CTTCAGTGCT 1260
AAGGGTGTGG CTAGTGTTTG TGTGGAAGAC TGGAATAACA
GGAAGGAATT TGTGTGTAAT 1320
GTGACTCACA GGGATCTGCC TTCACCACAG AAGAAATTCA

TCTCAAAACC CAATGAGGTG 1380
CACAAACATC CACCTGCTGT GTACCTGCTG CCACCAGCTC
GTGAGCAACT GAACCTGAGG 1440
GAGTCAGCCA CAGTCACCTG CCTGGTGAAG GGCTTCTCTC
CTGCAGACAT CAGTGTGCAG 1500
TGGCTTCAGA GAGGGCAACT CTTGCCCAA GAGAAGTATG
TGACCAGTGC CCCGATGCCA 1560
GAGCCTGGGG CCCAGGCTT CTACTTTACC CACAGCATCC
TGACTGTGAC AGAGGAGGAA 1620
TGGAACCTCCG GAGAGACCTA TACCTGTGTT GTAGGCCACG
AGGCCCTGCC ACACCTGGTG 1680
ACCGAGAGGA CCGTGGACAA GTCCACTGGT AAACCCACAC
TGTACAATGT CTCCTGATC 1740
ATGTCTGACA CAGGCGGCAC CTGCTATTGA CCAT 1774

TCTCAAAACC CAATGAGGTG 1380